STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _/0/527,438_

Source: _Pcr_

Date Processed by STIC: _2/10/06_

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PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO **REDUCE** ERRORED SEQUENCE LISTINGS, **PLEASE** USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
        http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

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Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission User Manual** - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

PCT

RAW SEQUENCE LISTING   DATE: 02/10/2006
PATENT APPLICATION: US/10/527,438   TIME: 08:40:50

Input Set : **A:\3fpo-07-05_sequence2.txt**
Output Set: **N:\CRF4\02102006\J527438.raw**

```
     3 <110> APPLICANT: Korea Research Institute of Bioscience and Biotechnology
     5 <120> TITLE OF INVENTION: Method for screening of a lipase having improved
enzymatic
     6         activity using yeast surface display vector and the lipase
     8 <130> FILE REFERENCE: 3fpo-07-05
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/527,438
C--> 10 <141> CURRENT FILING DATE: 2005-03-11
    10 <150> PRIOR APPLICATION NUMBER: KR 2002-55575
    11 <151> PRIOR FILING DATE: 2002-09-13
    13 <160> NUMBER OF SEQ ID NOS: 18
    15 <170> SOFTWARE: KopatentIn 1.71
```

ERRORED SEQUENCES

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    82 <210> SEQ ID NO: 6
    83 <211> LENGTH: 1023
    84 <212> TYPE: DNA
    85 <213> ORGANISM: Candida antarctica
    87 <220> FEATURE:
    88 <221> NAME/KEY: sig_peptide
    89 <222> LOCATION: (-51)..(-1)
    90 <223> OTHER INFORMATION: secretion signal
    93 <400> SEQUENCE: 6
E--> 94
atgaatatat tttacatatt tttgtttttg ctgtcattcg ttcaaggtac cgccactccc
E--> 96
ttggtgaagc gtctgccttc cggttcggac cctgcctttt cgcagcccaa gtcggtgctc
E--> 98
gatgcgggtc tgacctgcca gggtgcttcg ccatcctcgg tctccaaacc catccttctc
E--> 100
gtccccggaa ccggcaccac aggtccacag tcgttcgact cgaactggat ccccctctct    189
E--> 102
gcgcagctgg gttacacacc ctgctggatc tcacccccgc cgttcatgct caacgacacc    249
E--> 104
caggtcaaca cggagtacat ggtcaacgcc atcaccacgc tctacgctgg ttcgggcaac    309
E--> 106
aacaagcttc ccgtgctcac ctggtcccag ggtggtctgg ttgcacagtg gggtctgacc    369
E--> 108
ttcttcccca gtatcaggtc caaggtcgat cgacttatgg cctttgcgcc cgactacaag    429
E--> 110
ggcaccgtcc tcgccggccc tctcgatgca ctcgcggtta gtgcaccctc cgtatggcag    489
E--> 112
caaaccaccg gttcggcact cactaccgca ctccgaaacg caggtggtct gacccagatc    549
```

```
E--> 114
gtgcccacca ccaacctcta ctcggcgacc gacgagatcg ttcagcctca ggtgtccaac     609
E--> 116
tcgccactcg actcatccta cctcttcaac gggaagaacg tccaggcaca ggctgtgtgt     669
E--> 118
gggccgctgt tcgtcatcga ccatgcaggc tcgctcacct cgcagttctc ctacgtcgtc     729
E--> 120
ggtcgatccg ccctgcgctc caccacgggc caggctcgta gtgcagacta tggcattacc     789
E--> 122
gactgcaacc ctcttcccgc caatgatctg actcccgagc aaaaggtcgc cgcggctgcg     849
E--> 124
ctcccggcgc cggcggctgc agccatcgtg gcgggtccaa agcagaactg cgagcccgac     909
E--> 126
ctcatgccct acgcccgccc ctttgcagta ggcaaaagga cctgctccgg catcgtcacc     969
E--> 128
ccc                                                                   972
     131 <210> SEQ ID NO: 7
     132 <211> LENGTH: 1023
```

nos.

```
      133 <212> TYPE: DNA
      134 <213> ORGANISM: Candida antarctica
      136 <220> FEATURE:
      137 <221> NAME/KEY: sig_peptide
      138 <222> LOCATION: (-51)..(-1)
      139 <223> OTHER INFORMATION: secretion signal
      142 <400> SEQUENCE: 7
E--> 143
atgaatatat tttacatatt tttgtttttg ctgtcattcg ttcaaggtac cgccactcct            9
E--> 145
ttggtgaagc gtctgccttc cggttcggac cctgccttt cgcagcccaa gtcggtgctc           69
E--> 147
gatgcgggtc tgacctgcca aggtgcttcg ccatcctcgg tctccaaacc catccttctc          129
E--> 149
gtccccggaa ccggcaccac aggtccacag tcgttcgact cgaactggat ccccctctct          189
E--> 151
gcgcagctgg gttacacacc ctgctggatc tcaccccgc cgttcatgct caacgacacc           249
E--> 153
caggtcaaca cggagtacat ggtcaacgcc atcaccacgc tctacgctgg ttcgggcaac          309
E--> 155
aacaagcttc ccgtgctcac ctggtcccag ggtggtctgg ttgcacagtg gggtctgacc          369
E--> 157
ttcttcccca gtatcaggtc caaggtcgat cgacttatgg cctttgcgcc cgactacaag          429
E--> 159
ggcaccgtcc tcgccggccc tctcgatgca ctcgcggtta gtgcaccctc cgtatggcag          489
E--> 161
caaaccaccg gttcggcact cactaccgca ctccgaaacg caggtggtct gacccagatc          549
E--> 163
gtgcccacca ccaacctcta ctcggcgacc gacgagatcg ttcagcctca ggtgtccaac          609
E--> 165
tcgccactcg actcatccta ccttttcaac ggaaagaacg tccaggcaca ggctgtgtgt          669
E--> 167
gggccgcagt tcgtcatcga ccatgcaggc tcgctcacct cgcagttctc ctacgtcgtc          729
E--> 169
ggtcgatccg ccctgcgctc caccacgggc caggctcgta gtgcggacta tggcattacg          789
E--> 171
gactgcaacc ctcttcccgc caatgatctg actcccgagc aaaaggtcgc cgcggctgcg          849
E--> 173
ctcccggcgc cggcggctgc agccatcgtg gcgggtccaa agcagaactg cgagcccgac          909
E--> 175
ctcatgccct acgcccgccc ctttgcagta ggcaaaagga cctgctccgg catcgtcacc          969
E--> 177
ccc                                                                        972
      180 <210> SEQ ID NO: 8
      181 <211> LENGTH: 1023
      182 <212> TYPE: DNA
      183 <213> ORGANISM: Candida antarctica
      185 <220> FEATURE:
      186 <221> NAME/KEY: sig_peptide
      187 <222> LOCATION: (-51)..(-1)
      188 <223> OTHER INFORMATION: secretion signal
      191 <400> SEQUENCE: 8
E--> 192
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```
atgaatatat tttacatatt tttgtttttg ctgtcattcg ttcaaggtac cgccactcct     9
E--> 194
ttggtgaagc gtctgccttc cggttcggac cctgcctttt cgcagcccaa gtcggtgctc    69
E--> 196
gatgcgggtc tgacctgcca gggtgcttcg ccatcctcgg tctccaaacc catccttctc   129
E--> 198
gtccccggaa ccggcaccac aggtccacag tcgttcgact cgaactggat ccccctctct   189
E--> 200
gcgcagctgg gttacacacc ctgctggatc tcacccccgc cgttcatgct caacgacacc   249
E--> 202
caggtcaaca cggagtacat ggtcaacgcc atcaccacgc tctacgctgg ttcgggcaac   309
E--> 204
aacaagcttc ccgtgctcac ctggtcccag ggtggtctgg ttgcacagtg gggtctgacc   369
E--> 206
ttcttcccca gtatcaggtc caaggtcgat cgacttatgg cctttgcgcc cgactacaag   429
E--> 208
ggcaccgtcc tcgccggccc tctcgatgca ctcgcggtta gtgcaccctc cgtatggcag   489
E--> 210
caaaccaccg gttcggcact cactaccgca ctccgaaacg caggtggtct gacccagatc   549
E--> 212
gtgcccacca ccaacctcta ctcggcgacc gacgagatcg ttcagcctca ggtgtccaac   609
E--> 214
tcgccactcg actcatccta cctcttcaac ggaaagaacg tccaggcaca ggctgtgtgt   669
E--> 216
gggccgcagt tcgtcatcga ccatgcaggc tcgctcacct cgcagttctc ctacgtcgtc   729
E--> 218
ggtcgatccg ccctgcgctc caccacgggc caggctcgta gtgcagacta tggcattacg   789
E--> 220
gactgcaacc ctcttcccgc caatgatctg actcccgagc aaaaggtcgc cgcggctgcg   849
```

Input Set : A:\3fpo-07-05_sequence2.txt
Output Set: N:\CRF4\02102006\J527438.raw

```
E--> 222
ctcctggcgc cggcggctgc agccatcgtg gcgggtccaa agcagaactg cgagcccgac        909
E--> 224
ctcatgccct acgcccgccc ctttgcagta ggcaaaagga cctgctccgg catcgtcacc        969
E--> 226
ccc                                                                      972
```

same (handwritten)

```
     229 <210> SEQ ID NO: 9
     230 <211> LENGTH: 341
     231 <212> TYPE: PRT
     232 <213> ORGANISM: Candida antarctica
     234 <220> FEATURE:
     235 <221> NAME/KEY: SIGNAL
     236 <222> LOCATION: (-24)..(-8)
     237 <223> OTHER INFORMATION: secretion signal
     240 <400> SEQUENCE: 9
     241 Met Asn Ile Phe Tyr Ile Phe Leu Phe Leu Leu Ser Phe Val Gln Gly
     242 -24          -20              -15              -10
     244 Thr Ala Thr Pro Leu Val Lys Arg Leu Pro Ser Gly Ser Asp Pro Ala
E--> 245          -5               1               5    6
     247 Phe Ser Gln Pro Lys Ser Val Leu Asp Ala Gly Leu Thr Cys Gln Gly
     248      10  11           15  16              20  21
     250 Ala Ser Pro Ser Ser Val Ser Lys Pro Ile Leu Leu Val Pro Gly Thr
     251      26               31              36
     253 Gly Thr Thr Gly Pro Gln Ser Phe Asp Ser Asn Trp Ile Pro Leu Ser
     254 41               46              51              56
     256 Ala Gln Leu Gly Tyr Thr Pro Cys Trp Ile Ser Pro Pro Pro Phe Met
     257          61              66              71
     259 Leu Asn Asp Thr Gln Val Asn Thr Glu Tyr Met Val Asn Ala Ile Thr
     260          76              81              86
     262 Thr Leu Tyr Ala Gly Ser Gly Asn Asn Lys Leu Pro Val Leu Thr Trp
     263      91              96              101
     265 Ser Gln Gly Gly Leu Val Ala Gln Trp Gly Leu Thr Phe Phe Pro Ser
     266      106             111             116
     268 Ile Arg Ser Lys Val Asp Arg Leu Met Ala Phe Ala Pro Asp Tyr Lys
     269 121             126             131             136
     271 Gly Thr Val Leu Ala Gly Pro Leu Asp Ala Leu Ala Val Ser Ala Pro
     272          141             146             151
     274 Ser Val Trp Gln Gln Thr Thr Gly Ser Ala Leu Thr Thr Ala Leu Arg
     275      156             161             166
     277 Asn Ala Gly Gly Leu Thr Gln Ile Val Pro Thr Thr Asn Leu Tyr Ser
     278      171             176             181
     280 Ala Thr Asp Glu Ile Val Gln Pro Gln Val Ser Asn Ser Pro Leu Asp
     281      186             191             196
     283 Ser Ser Tyr Leu Phe Asn Gly Lys Asn Val Gln Ala Gln Ala Val Cys
     284 201             206             211             216
     286 Gly Pro Leu Phe Val Ile Asp His Ala Gly Ser Leu Thr Ser Gln Phe
     287          221             226             231
     289 Ser Tyr Val Val Gly Arg Ser Ala Leu Arg Ser Thr Thr Gly Gln Ala
     290      236             241             246
     292 Arg Ser Ala Asp Tyr Gly Ile Thr Asp Cys Asn Pro Leu Pro Ala Asn
     293      251             256             261
     295 Asp Leu Thr Pro Glu Gln Lys Val Ala Ala Ala Ala Leu Pro Ala Pro
```

(handwritten notes, right margin): invalid numbering number the amino acids under every 5 amino acids

RAW SEQUENCE LISTING   DATE: 02/10/2006
PATENT APPLICATION: US/10/527,438   TIME: 08:40:50

Input Set : **A:\3fpo-07-05_sequence2.txt**
Output Set: **N:\CRF4\02102006\J527438.raw**

```
296    266                271                276                    Numbering
298 Ala Ala Ala Ala Ile Val Ala Gly Pro Lys Gln Asn Cys Glu Pro Asp   off
299 281                286                291                296
301 Leu Met Pro Tyr Ala Arg Pro Phe Ala Val Gly Lys Arg Thr Cys Ser
302            301                306                311
304 Gly Ile Val Thr Pro
305            316
308 <210> SEQ ID NO: 10
309 <211> LENGTH: 341
310 <212> TYPE: PRT
311 <213> ORGANISM: Candida antarctica
313 <220> FEATURE:
314 <221> NAME/KEY: SIGNAL
315 <222> LOCATION: (-24)..(-8)
316 <223> OTHER INFORMATION: secretion signal
319 <400> SEQUENCE: 10
320 Met Asn Ile Phe Tyr Ile Phe Leu Phe Leu Leu Ser Phe Val Gln Gly
321 -24             -20                -15                -10
323 Thr Ala Thr Pro Leu Val Lys Arg Leu Pro Ser Gly Ser Asp Pro Ala
324            -5                 1                  6                  same
326 Phe Ser Gln Pro Lys Ser Val Leu Asp Ala Gly Leu Thr Cys Gln Gly   errors
327         11                16                21
329 Ala Ser Pro Ser Ser Val Ser Lys Pro Ile Leu Leu Val Pro Gly Thr
330     26                31                36
332 Gly Thr Thr Gly Pro Gln Ser Phe Asp Ser Asn Trp Ile Pro Leu Ser
333 41                46                51                          56
335 Ala Gln Leu Gly Tyr Thr Pro Cys Trp Ile Ser Pro Pro Pro Phe Met
336            61                66                71
338 Leu Asn Asp Thr Gln Val Asn Thr Glu Tyr Met Val Asn Ala Ile Thr
339            76                81                86
341 Thr Leu Tyr Ala Gly Ser Gly Asn Asn Lys Leu Pro Val Leu Thr Trp
342         91                96                101
344 Ser Gln Gly Gly Leu Val Ala Gln Trp Gly Leu Thr Phe Phe Pro Ser
345     106               111               116
347 Ile Arg Ser Lys Val Asp Arg Leu Met Ala Phe Ala Pro Asp Tyr Lys
348 121               126               131                       136
350 Gly Thr Val Leu Ala Gly Pro Leu Asp Ala Leu Ala Val Ser Ala Pro
351            141               146               151
353 Ser Val Trp Gln Gln Thr Thr Gly Ser Ala Leu Thr Thr Ala Leu Arg
354            156               161               166
356 Asn Ala Gly Gly Leu Thr Gln Ile Val Pro Thr Thr Asn Leu Tyr Ser
357         171               176               181
359 Ala Thr Asp Glu Ile Val Gln Pro Gln Val Ser Asn Ser Pro Leu Asp
360     186               191               196
362 Ser Ser Tyr Leu Phe Asn Gly Lys Asn Val Gln Ala Gln Ala Val Cys
363 201               206               211                       216
365 Gly Pro Gln Phe Val Ile Asp His Ala Gly Ser Leu Thr Ser Gln Phe
366            221               226               231
368 Ser Tyr Val Val Gly Arg Ser Ala Leu Arg Ser Thr Thr Gly Gln Ala
```

E--> 324

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/527,438

DATE: 02/10/2006
TIME: 08:40:50

Input Set : A:\3fpo-07-05_sequence2.txt
Output Set: N:\CRF4\02102006\J527438.raw

```
369            236            241            246
371 Arg Ser Ala Asp Tyr Gly Ile Thr Asp Cys Asn Pro Leu Pro Ala Asn
372        251            256            261
374 Asp Leu Thr Pro Glu Gln Lys Val Ala Ala Ala Ala Leu Pro Ala Pro
375        266            271            276
377 Ala Ala Ala Ala Ile Val Ala Gly Pro Lys Gln Asn Cys Glu Pro Asp
378 281            286            291            296
380 Leu Met Pro Tyr Ala Arg Pro Phe Ala Val Gly Lys Arg Thr Cys Ser
381            301            306            311
383 Gly Ile Val Thr Pro
384        316
387 <210> SEQ ID NO: 11
388 <211> LENGTH: 341
389 <212> TYPE: PRT
390 <213> ORGANISM: Candida antarctica
392 <220> FEATURE:
393 <221> NAME/KEY: SIGNAL
394 <222> LOCATION: (-24)..(-1)
395 <223> OTHER INFORMATION: secretion signal
398 <400> SEQUENCE: 11
399 Met Asn Ile Phe Tyr Ile Phe Leu Phe Leu Leu Ser Phe Val Gln Gly
400 -24            -20            -15            -10
402 Thr Ala Thr Pro Leu Val Lys Arg Leu Pro Ser Gly Ser Asp Pro Ala
403            -5             1              6
405 Phe Ser Gln Pro Lys Ser Val Leu Asp Ala Gly Leu Thr Cys Gln Gly
406        11             16             21
408 Ala Ser Pro Ser Ser Val Ser Lys Pro Ile Leu Leu Val Pro Gly Thr
409        26             31             36
411 Gly Thr Thr Gly Pro Gln Ser Phe Asp Ser Asn Trp Ile Pro Leu Ser
412 41             46             51             56
414 Ala Gln Leu Gly Tyr Thr Pro Cys Trp Ile Ser Pro Pro Pro Phe Met
415            61             66             71
417 Leu Asn Asp Thr Gln Val Asn Thr Glu Tyr Met Val Asn Ala Ile Thr
418            76             81             86
420 Thr Leu Tyr Ala Gly Ser Gly Asn Asn Lys Leu Pro Val Leu Thr Trp
421        91             96             101
423 Ser Gln Gly Gly Leu Val Ala Gln Trp Gly Leu Thr Phe Phe Pro Ser
424        106            111            116
426 Ile Arg Ser Lys Val Asp Arg Leu Met Ala Phe Ala Pro Asp Tyr Lys
427 121            126            131            136
429 Gly Thr Val Leu Ala Gly Pro Leu Asp Ala Leu Ala Val Ser Ala Pro
430            141            146            151
432 Ser Val Trp Gln Gln Thr Thr Gly Ser Ala Leu Thr Thr Ala Leu Arg
433            156            161            166
435 Asn Ala Gly Gly Leu Thr Gln Ile Val Pro Thr Thr Asn Leu Tyr Ser
436            171            176            181
438 Ala Thr Asp Glu Ile Val Gln Pro Gln Val Ser Asn Ser Pro Leu Asp
439        186            191            196
441 Ser Ser Tyr Leu Phe Asn Gly Lys Asn Val Gln Ala Gln Ala Val Cys
```

E--> 403

Jane (signature)

Jane (signature)

RAW SEQUENCE LISTING   DATE: 02/10/2006
PATENT APPLICATION: US/10/527,438   TIME: 08:40:50

Input Set : **A:\3fpo-07-05_sequence2.txt**
Output Set: **N:\CRF4\02102006\J527438.raw**

```
442 201                  206                 211                 216
444 Gly Pro Gln Phe Val Ile Asp His Ala Gly Ser Leu Thr Ser Gln Phe
445                  221                 226                 231
447 Ser Tyr Val Val Gly Arg Ser Ala Leu Arg Ser Thr Thr Gly Gln Ala
448       ·          236         ·        241       ·  ·      246
450 Arg Ser Ala Asp Tyr Gly Ile Thr Asp Cys Asn Pro Leu Pro Ala Asn
451       251                 256                 261
453 Asp Leu Thr Pro Glu Gln Lys Val Ala Ala Ala Ala Leu Leu Ala Pro
454       266                 271                 276
456 Ala Ala Ala Ala Ile Val Ala Gly Pro Lys Gln Asn Cys Glu Pro Asp
457 281                  286                 291                 296
459 Leu Met Pro Tyr Ala Arg Pro Phe Ala Val Gly Lys Arg Thr Cys Ser
460                  301                 306                 311
462 Gly Ile Val Thr Pro
463                  316
602 <210> SEQ ID NO: 18
603 <211> LENGTH: 29
604 <212> TYPE: DNA
605 <213> ORGANISM: Artificial Sequence
607 <220> FEATURE:
608 <223> OTHER INFORMATION: LP35 primer
611 <400> SEQUENCE: 18
612
```

ctgcagccgc cggcgccggg agcgcagcc   29

```
E--> 615 Pct/kr03/01820
E--> 616 rO/kr   04.11.2003
E--> 622 1
```

(handwritten: same)

(handwritten annotation, circled: delete at end of file)

VERIFICATION SUMMARY   DATE: 02/10/2006
PATENT APPLICATION: **US/10/527,438**   TIME: 08:40:51

Input Set : **A:\3fpo-07-05_sequence2.txt**
Output Set: **N:\CRF4\02102006\J527438.raw**

```
L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:94 M:254 E: No. of Bases conflict, LENGTH:Input:9 Counted:60 SEQ:6
L:96 M:254 E: No. of Bases conflict, LENGTH:Input:69 Counted:120 SEQ:6
L:98 M:254 E: No. of Bases conflict, LENGTH:Input:129 Counted:180 SEQ:6
L:100 M:254 E: No. of Bases conflict, LENGTH:Input:189 Counted:240 SEQ:6
L:102 M:254 E: No. of Bases conflict, LENGTH:Input:249 Counted:300 SEQ:6
L:104 M:254 E: No. of Bases conflict, LENGTH:Input:309 Counted:360 SEQ:6
L:106 M:254 E: No. of Bases conflict, LENGTH:Input:369 Counted:420 SEQ:6
L:108 M:254 E: No. of Bases conflict, LENGTH:Input:429 Counted:480 SEQ:6
L:110 M:254 E: No. of Bases conflict, LENGTH:Input:489 Counted:540 SEQ:6
L:112 M:254 E: No. of Bases conflict, LENGTH:Input:549 Counted:600 SEQ:6
L:114 M:254 E: No. of Bases conflict, LENGTH:Input:609 Counted:660 SEQ:6
L:116 M:254 E: No. of Bases conflict, LENGTH:Input:669 Counted:720 SEQ:6
L:118 M:254 E: No. of Bases conflict, LENGTH:Input:729 Counted:780 SEQ:6
L:120 M:254 E: No. of Bases conflict, LENGTH:Input:789 Counted:840 SEQ:6
L:122 M:254 E: No. of Bases conflict, LENGTH:Input:849 Counted:900 SEQ:6
L:124 M:254 E: No. of Bases conflict, LENGTH:Input:909 Counted:960 SEQ:6
L:126 M:254 E: No. of Bases conflict, LENGTH:Input:969 Counted:1020 SEQ:6
L:128 M:254 E: No. of Bases conflict, LENGTH:Input:972 Counted:1023 SEQ:6
L:143 M:254 E: No. of Bases conflict, LENGTH:Input:9 Counted:60 SEQ:7
L:145 M:254 E: No. of Bases conflict, LENGTH:Input:69 Counted:120 SEQ:7
L:147 M:254 E: No. of Bases conflict, LENGTH:Input:129 Counted:180 SEQ:7
L:149 M:254 E: No. of Bases conflict, LENGTH:Input:189 Counted:240 SEQ:7
L:151 M:254 E: No. of Bases conflict, LENGTH:Input:249 Counted:300 SEQ:7
L:153 M:254 E: No. of Bases conflict, LENGTH:Input:309 Counted:360 SEQ:7
L:155 M:254 E: No. of Bases conflict, LENGTH:Input:369 Counted:420 SEQ:7
L:157 M:254 E: No. of Bases conflict, LENGTH:Input:429 Counted:480 SEQ:7
L:159 M:254 E: No. of Bases conflict, LENGTH:Input:489 Counted:540 SEQ:7
L:161 M:254 E: No. of Bases conflict, LENGTH:Input:549 Counted:600 SEQ:7
L:163 M:254 E: No. of Bases conflict, LENGTH:Input:609 Counted:660 SEQ:7
L:165 M:254 E: No. of Bases conflict, LENGTH:Input:669 Counted:720 SEQ:7
L:167 M:254 E: No. of Bases conflict, LENGTH:Input:729 Counted:780 SEQ:7
L:169 M:254 E: No. of Bases conflict, LENGTH:Input:789 Counted:840 SEQ:7
L:171 M:254 E: No. of Bases conflict, LENGTH:Input:849 Counted:900 SEQ:7
L:173 M:254 E: No. of Bases conflict, LENGTH:Input:909 Counted:960 SEQ:7
L:175 M:254 E: No. of Bases conflict, LENGTH:Input:969 Counted:1020 SEQ:7
L:177 M:254 E: No. of Bases conflict, LENGTH:Input:972 Counted:1023 SEQ:7
L:192 M:254 E: No. of Bases conflict, LENGTH:Input:9 Counted:60 SEQ:8
L:194 M:254 E: No. of Bases conflict, LENGTH:Input:69 Counted:120 SEQ:8
L:196 M:254 E: No. of Bases conflict, LENGTH:Input:129 Counted:180 SEQ:8
L:198 M:254 E: No. of Bases conflict, LENGTH:Input:189 Counted:240 SEQ:8
L:200 M:254 E: No. of Bases conflict, LENGTH:Input:249 Counted:300 SEQ:8
L:202 M:254 E: No. of Bases conflict, LENGTH:Input:309 Counted:360 SEQ:8
L:204 M:254 E: No. of Bases conflict, LENGTH:Input:369 Counted:420 SEQ:8
L:206 M:254 E: No. of Bases conflict, LENGTH:Input:429 Counted:480 SEQ:8
L:208 M:254 E: No. of Bases conflict, LENGTH:Input:489 Counted:540 SEQ:8
L:210 M:254 E: No. of Bases conflict, LENGTH:Input:549 Counted:600 SEQ:8
```

VERIFICATION SUMMARY   DATE: 02/10/2006
PATENT APPLICATION: **US/10/527,438**   TIME: 08:40:51

Input Set : **A:\3fpo-07-05_sequence2.txt**
Output Set: **N:\CRF4\02102006\J527438.raw**

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L:212 M:254 E: No. of Bases conflict, LENGTH:Input:609 Counted:660 SEQ:8
L:214 M:254 E: No. of Bases conflict, LENGTH:Input:669 Counted:720 SEQ:8
L:216 M:254 E: No. of Bases conflict, LENGTH:Input:729 Counted:780 SEQ:8
L:218 M:254 E: No. of Bases conflict, LENGTH:Input:789 Counted:840 SEQ:8
L:220 M:254 E: No. of Bases conflict, LENGTH:Input:849 Counted:900 SEQ:8
L:222 M:254 E: No. of Bases conflict, LENGTH:Input:909 Counted:960 SEQ:8
L:224 M:254 E: No. of Bases conflict, LENGTH:Input:969 Counted:1020 SEQ:8
L:226 M:254 E: No. of Bases conflict, LENGTH:Input:972 Counted:1023 SEQ:8
L:245 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9
L:324 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10
L:403 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:11
L:615 M:254 E: No. of Bases conflict, LENGTH:Input:1820 Counted:36 SEQ:18
L:615 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:5
L:615 M:112 C: (48) String data converted to lower case,
L:616 M:254 E: No. of Bases conflict, LENGTH:Input:2003 Counted:43 SEQ:18
L:616 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:8
L:616 M:112 C: (48) String data converted to lower case,
L:622 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:622 M:252 E: No. of Seq. differs, <211> LENGTH:Input:29 Found:43 SEQ:18
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